

pQE-30, pQE-31, and pQE-32 Vectors

Positions of elements in bases	pQE-30	pQE-31	pQE-32
Vector size (bp)	3461	3463	3462
Start of numbering at <i>Xho</i> I (CTCGAG)	1-6	1-6	1-6
T5 promoter/lac operator element	7-87	7-87	7-87
T5 transcription start	61	61	61
6xHis-tag coding sequence	127-144	127-144	127-144
Multiple cloning site	145-192	147-194	146-193
Lambda <i>t</i> ₀ transcriptional termination region	208-302	210-304	209-303
<i>rrnB</i> T1 transcriptional termination region	1064-1162	1066-1164	1065-1163
ColE1 origin of replication	1638	1640	1639
β -lactamase coding sequence	3256-2396	3258-2398	3257-2397

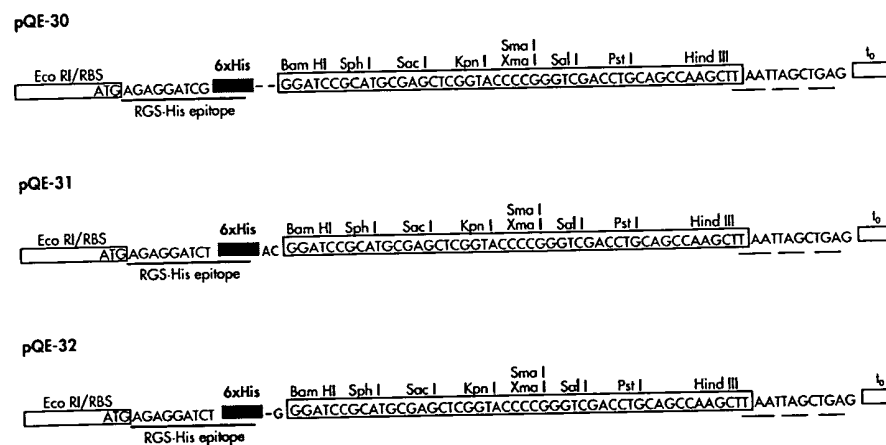
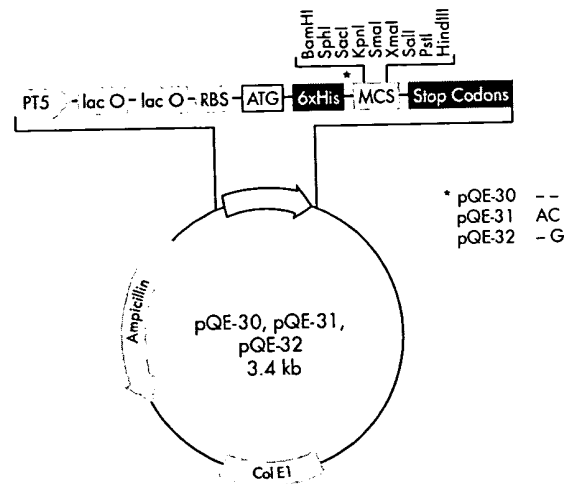


Figure 1

FIGURE 2

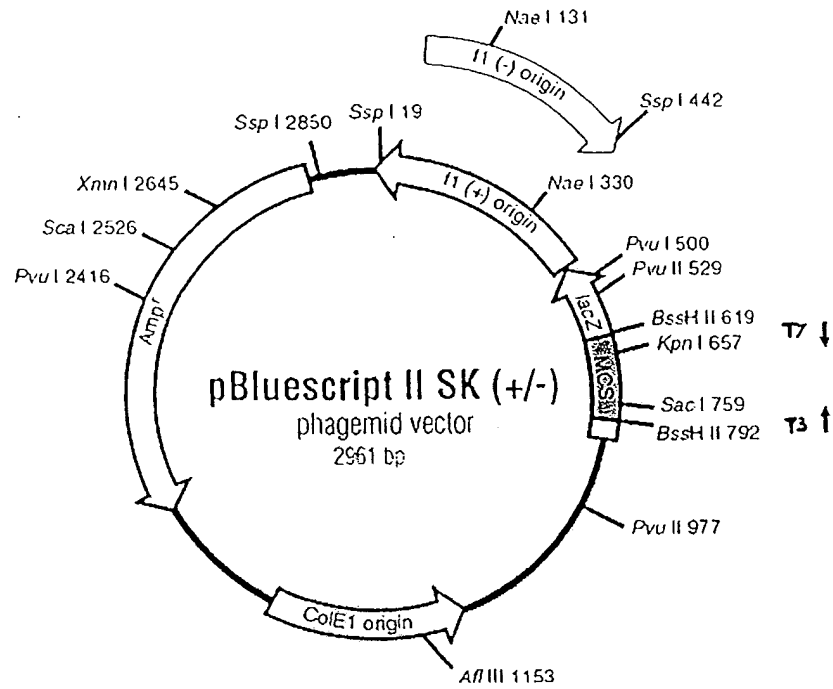
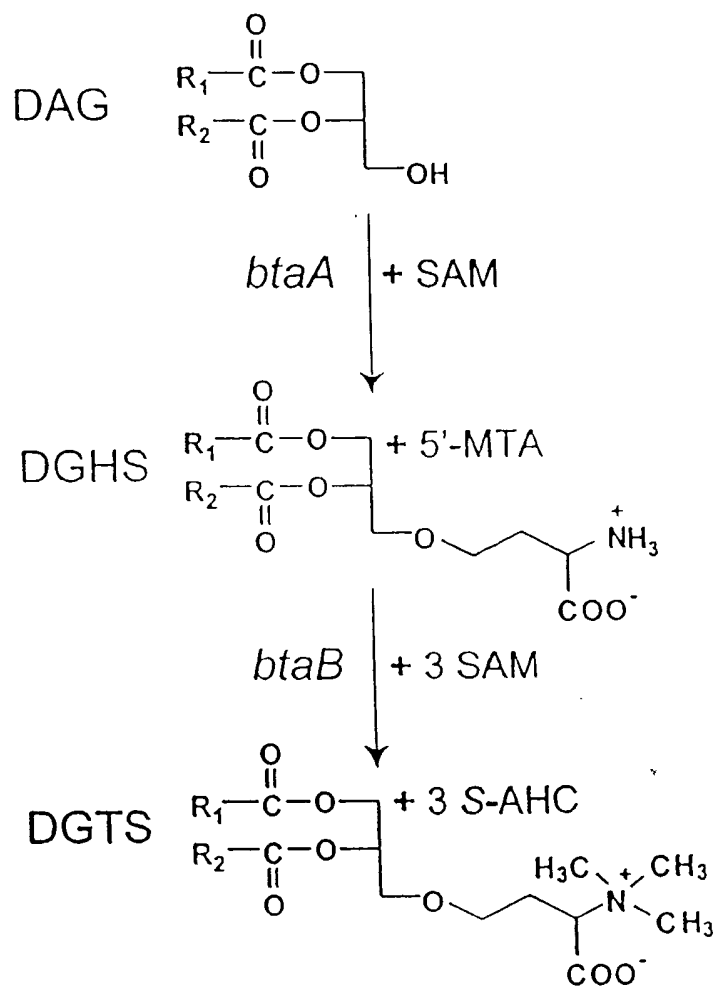


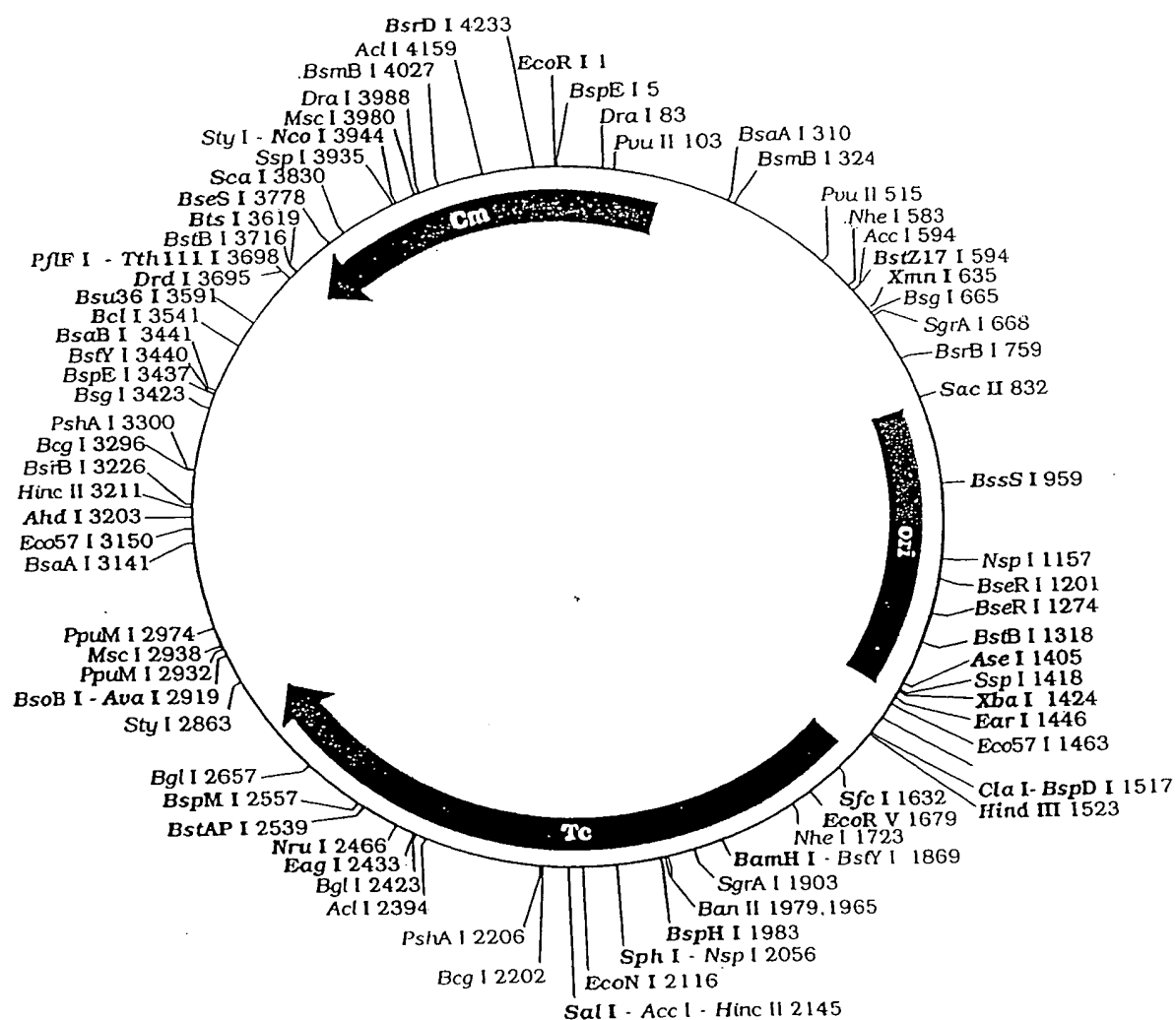
FIGURE 3



pACYC184

4,244 base pairs
GenBank Accession / X06403

FIGURE 4



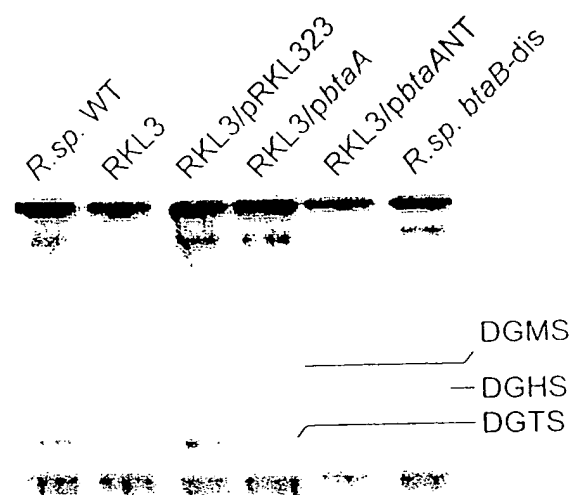


FIGURE 5

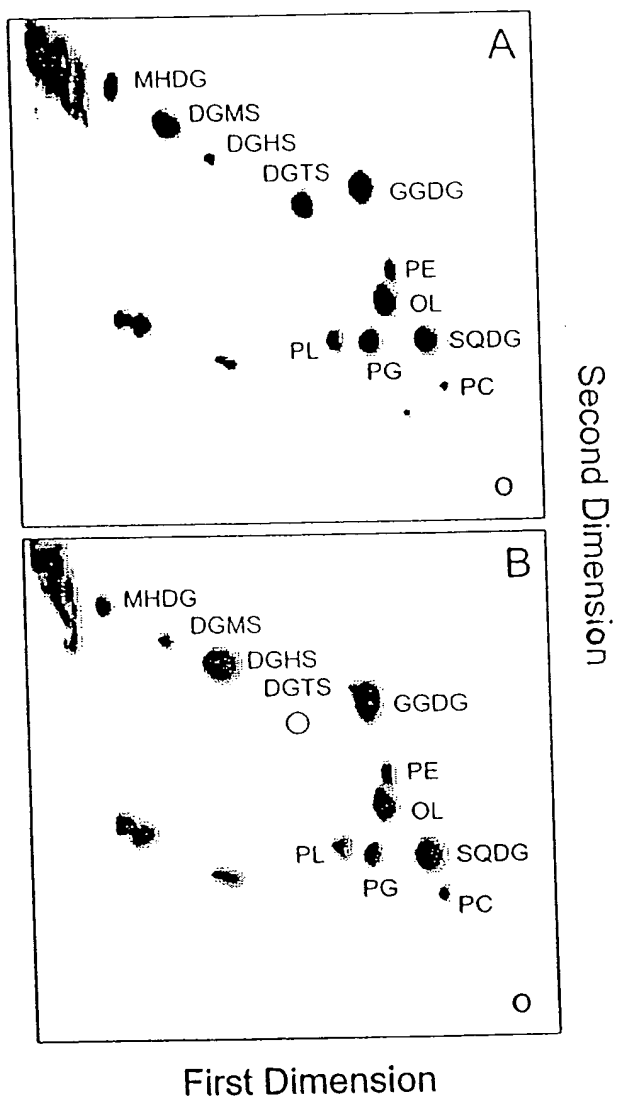


FIGURE 6

FIGURE 7

btaA gene cDNA Sequence

1-57 gtgacgc agttcgccct caccacactg cccgccccgc cggttgcccc ccagatcggc
58-117 gccgccgtgc accgcacgtc gcttctcagc gccgaaggac tgatggagcg gatgttctcg
118-177 cgcctcttcc acggcctcgt ctatccgcag atctgggagg atccggcggt ggacatggcg
178-237 gccctcgcca tccgccccgg ggaccggctg gtggccatcg cctcgggcgg ttgcaacgtg
238-297 ctttcctatc tcacgcaggg gccgggctcg atcctcgccg tggatctctc gcccgcccat
298-357 gtggcgctgg ggcggtgaa gctcgccgcc gcgcggacgc tgcccgacca tgccgccttc
358-417 ttcgaatctc tcggtcgcgc agacctgccc ggcaatgcgg ccctctacga ccgcacatc
418-477 gcgcccgcgc tcgacggccg gagccgccgc tactgggagg cgcgcagccc cttcggccgg
478-537 cgcatccagc tgttcgagcg cggcttctac cggcacggtg ccctcggccg cttcacggcg
538-597 gcggcccata cgctcgcgcg ggccgcgggc accgacctgc ggggctttct cgactgtccc
598-657 gacatcgagg cgcagcgag ctctcttac gcccatatcg ggccgctctt cgaggcgccc
658-717 gtggtgcagg cgctcgcccc acggccggcc gcgctcttcg ggctggggat cccgcccgcg
718-777 caatatgcgc ttctggcggg agacggcgac ggcgacgtgc tgccggtgct gcgccagcgc
778-837 ctccaccggc tgctctgtga ctccccctg cgcgagaact acttcgcctt ccaggccatc
838-897 gcccgcgct atccgcggcc cggcgagggc gcgctgccgc cctatctcga acccaccgcc
898-957 ttcgagacgc tgcgcgagaa cgcgggccgg gtgcagatcg agaaccgcag cctgaccgag
958-1017 gcgctcgcgg ccgaaccga ggagagcatc cacggcttca ccctgctcga tgcgcaggac
1018-1077 tggaatgacgg acgcgcagct gaccgcgctc tggcggcagg tgacgcgcac tgcagcgccc
1078-1137 ggcgcgcggg tgatcttccg caccggcggg gcggccgacc tgctgcccggccgagtgcc
1138-1197 gaggagatcc tcgggcactg gcgcgccgac cgggcggcgg gacaggcggg ccatgccgcc
1198-1252 gaccgttcgg cgatctacgg cggcttccac ctctaccggc ggagggacgc catga

FIGURE 8

btaB gene cDNA Sequence

1-60 atgaccgacg ccacccatgc ggcgctgatg gacgcgacct accgccacca gcgccggatc
61-120 tacgacgtca cgcggcggca ctctctgctc ggccgcgacc ggctgatcgc cgagctcgac
121-180 ccgccccccg gcgcccgggt gctcgagatc gcctgcggca cggggcgcaa cctcgacctg
181-240 atcgccgggc gctggcccgg ctgccggctc tcggggctcg acatctcgca ggagatgctg
240-300 gcctcgggcc gcgcgcgtct gggccggcgc gcgacgtgg cgctcggcga tgccaccggg
301-360 ttcgaggccc tgcccctctt cggcaccgac cggttcgagc ggatcgtcct ctctacgcg
361-420 ctctgatga tccccgactg gcgcgaggcc ctgcgtgagg cggcgcttca tctcgtgccg
421-480 ggggggcggc tgcattgctg cgacttcggc gatcaggcgg gcctgcccgg ctgggcccgc
481-540 gccggcctgc gcggctggat cgggcgcttc cacgtcacgc cgcgcgacga tctgggcacg
541-600 gcactgggcg aaacggcgct cgggatcggg ggctatgccg aataccggtc cctcggcggg
601-660 ggatatgcga ttctcggcac gctcacgcgg tgagagatcc cctgccctgc gcgtgacgt
661-720 tgtctgcccg caggcgaccg gccgcgcgac ggccggcctg cgggcgatcc ggcgcactga
721-780 aggcccggcg cgtcgcgcgc ggggacgtag cccgcagcgg caagcggccg acagagcctg
781-840 acagaccgtt cacggtgcgc gctccggatc ggggtgtggag ccggtgttc agaggtcagg
841-900 cctcgaggga aagccctctg gcccgacggg caaattgtcc gggatctcta atcgggaaat
901-960 tggtcggagc gagaggattc gaacctccga ccccctgctc ccgaagcagg tgcgtacca
961-1020 ggctgcgcta cgctccgacc ttggcgtgcg gattataggg tcgcgcatcc gaatgcaagg
1021-1080 gggtccgaac gcaattcgct acggagtgtc tcgcgtctcg cggcggcgca gaaggcgcgg
1081-1140 catgaggccc acctcgggcc gcaggcgcgt ctggctcgcc gggcggttct ccgacacgtt
1141-1200 gcggcgcat tcgcggccga cgatalagag gccgctcgcg atgatgacct ccgccccgac
1201-1255 ccagggtccag acgtcggacc gctcgccgaa gatgagccag ccgaagatcc ctgac

FIGURE 9

btaA gene Amino Acid Sequence

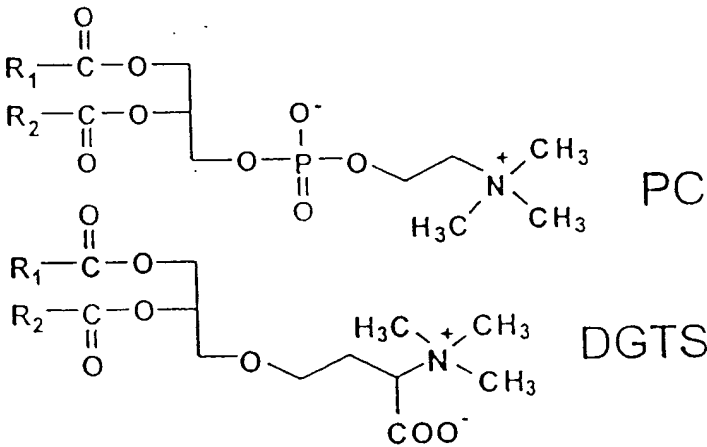
1-50 MTQFALTHLP APPVARQIGA AVHRTSLLSA EGLMERMFSS LFHGLVYPQI
51-100 WEDPAVDMAA LAIRPGDRLV AIASGGCNVL SYLTQGPGSI LAVDLSPAVAL
101-150 GRLKLAAART LPDHAAFFDL FGRADLPGNA ALYDRHIAPA LDGRSRRYWE
151-200 ARSPFGRRIQ LFERGFYRHG ALGRFIGAAH TLARAAGTDL RGFLDCPDIE
201-250 AQRSFFYAH I GPLFEAPVVQ ALARRPAALF GLGIPPAQYA LLAGDGDGDV
251-300 LPVLRQRLHR LLCDFPLREN YFAFQAIARR YPRPGEGALP PYLEPTAFET
301-350 LRENAGRVQI ENRSLTEALAA EPEESIHGFT LLDAQDWMTD AQLTALWRQV
351-400 TRTAAPGARV IFRTGGAADL LPGRVPPEIL GHWRADRAAG QAGHAADRSA
401-413 IYGGFHLYRR RDA

FIGURE 10

btaB gene Amino Acid Sequence

1-50 MTDATHAALM DATYRHQRRY YDVTRRHFL GRDLIAELD PPPGARVLEI
51-100 ACGTGRNLDL IGRRWPGCRL SGLDISQEML ASARARLGRR ATLALGDATR
101-150 FEALPLFGTD RFERIVLSYA LSMIPDWREA LREAALHLVP GGRLHVVDG
151-200 DQAGLPGWAR AGLRGWIGRF HVTPRDDLGT ALGETALGIG GYAEYRSLGG
201-210 GYAILGTLTR

FIGURE 11



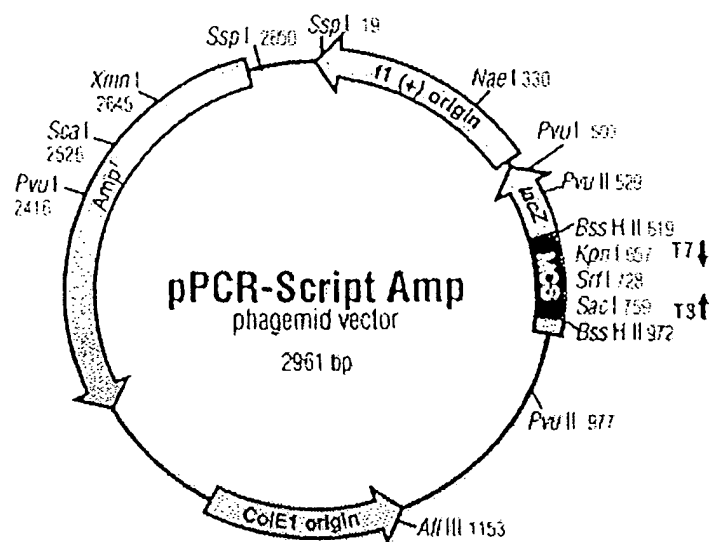


FIGURE 12

Comments for pYES2:
 5867 nucleotides

FIGURE 13

GAL1 promoter: bases 1-452
 T7 promoter/printing site: bases 476-495
 Multiple cloning site: bases 502-601
 CYC1 transcription terminator: bases 608-857
 pMB1 (pUC-derived) origin: bases 1039-1712
 Ampicillin resistance gene: bases 1857-2717
 URA3 gene: bases 2735-3842
 2 micron origin: bases 3840-5317
 f1 origin: bases 5385-5840

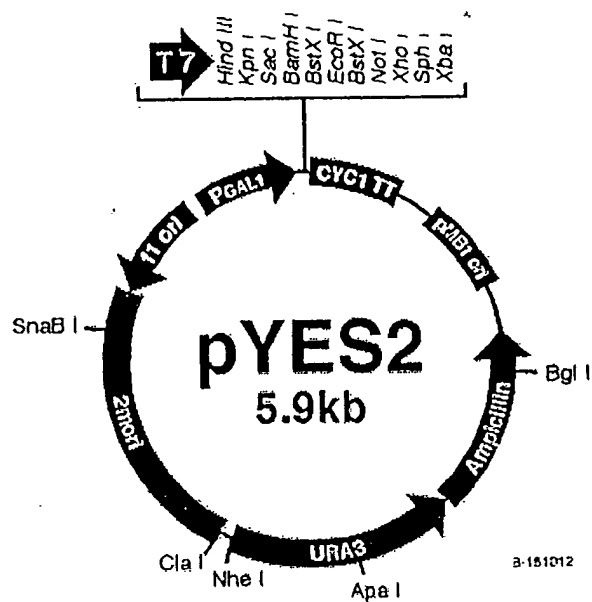


FIGURE 14

Mutagenesis Oligonucleotide btaA-L9I

5'-CGC CCT CAC CCA CAT TCC CGC CCC GC-3'

and its reverse complement:

5'-GCG GGG CGG GAA TGT GGG TGA GGG CG-3'

FIGURE 15

Mutagenesis Oligonucleotide btaA-A201G

5'-GAC TGT CCC GAG ATC GAG GGC CAG CGC CAG C-3'

and its reverse complement:

5'-GCT GGC GCT GGC CCT CGA TCT CGG GAC AGT C-3'

FIGURE 16

Mutagenesis Oligonucleotide btaA-S399T

5'-GCC GCC GAC CGT ACG GCG ATC TAC GG-3'

and its reverse complement:

5'-CCG TAG ATC GCC GTA CGG TCG GCG GC-3'

FIGURE 17

Mutagenesis Oligonucleotide btaB-T13S

5'-GCT GAT GGA CGC GTC CTA CCG CCA CCA G-3'

and its reverse complement:

5'-CTG GTG GCG GTA GGA CGC GTC CAT CAG C-3'

FIGURE 18

Mutagenesis Oligonucleotide btaB-I115L

5'-CGG TTC GAG CGG CTC GTC CTC TCC TAC GC-3'

and its reverse complement:

5'-GCG TAG GAG AGG ACG AGC CGC TCG AAC CG-3'

FIGURE 19

Mutagenesis Oligonucleotide btaB-G206A

5'-GGA TAT GCG ATT CTC GCC ACG CTC ACG CG-3'

and its reverse complement:

5'-CGC GTG AGC GTG GCG AGA ATC GCA TAT CC-3'

RsBtaA 1 MTQFALTHLPAPPVARQTCAAVHRTSLLSAEGEMERME SRLEHGLVYPQIWEEDPAVDMAA
 MlBtaA 1 MT--DVSSDLVFRRGKEVCKAVYQNRALSKAGISERLEAFLESGLVYPQIWEEDPDVDMBA
 consensus 1 mt lt ar iG AV LS Gl ERmF LF GLVYPQIWEEDP VDM A

RsBtaA 61 LAIRPGDRIVA IASGGCNVLSYLTQGPESILAVDLSPAHV ALGRUKLAAARTLPDHAFF
 MlBtaA 59 MGLGQGHRIIVT IASGGCNVLA YLTRSPARIDAVDLNAAHTALNRVKLEAVRRLLPSQGLF
 consensus 61 l i G RlV IASGGCNvL YLT Pg I AVDL AHvAL RlKL A R LP a F

RsBtaA 121 DLFCRADLPGNAALYDRHIAPALDGRSRYWEARSPPG-RRIOIFERGFYRHGALGRFIC
 MlBtaA 119 RFECADTSHNSQAYDRFIAPHLDPVSRHYWERRNWRGRRIAVEDRNFYOTGLGLFIA
 consensus 121 FG AD N YDR IAP LD SRyWE R G RRI lFeR FY G LG FIg

RsBtaA 180 AHTLARAAC TDLRGFLDCPDIEAQRSEFFYAHICPIFEAPVWQALARRPAALFGLGIPPA
 MlBtaA 179 MCHRTAKFFCVNPAHMM EARNIGEORFFNEEBAPVFDKKLWKWATSRKASLFGLGIPPA
 consensus 181 aH Ar G ld I QR FF igPlFe vv R A LFGLGIPPA

RsBtaA 240 QYALLAGDGDGVVFLRQRLHRLLCDFPLRENYFAFQA IARRYPRPGEALPPYLEPTA
 MlBtaA 239 QYDSLITS GDGTMASVLRARLEKLA CDFPLENNYFAWQAFARRYPNPGEAALPAYLEKQN
 consensus 241 QY L GDG v VLr RL rL CDFPL NYFAfQA ARRYP PGEgALP YLE

RsBtaA 300 FETIRENAGRVC IENRSLIEALAAPEESTHGFLLDAQDWMTDAQLTALWROVIRTAAP
 MlBtaA 299 YETIRGNIDRVAIHHANLIEFLAKDAGIVDRFILLDAQDWMTDDQLNALWSEISRTASA
 consensus 301 fetlR N RV I L E Laa si F LLDAQDWMTD QL ALW vtrTA

RsBtaA 360 GARVIFRTGG AADLLPGRVPEETLGHWRADRAAGQAGHAADRSATYGGFHLYRRRDA
 MlBtaA 359 GARVIFRTAAEPSLLPGRVSTSLDDWDYQDEASREFSARDRSATYGGFHLYVKRTA
 consensus 361 GARVIFRTgg LLPGRV iL W A A DRSAIYGGFHLY rR A

FIGURE 20

RsBtaB 1 -----MTDATHAALMDATYRHORRIYDVTRRHELLGRDRLLAELEPPPGARVLEIAC
 MlBtaB 1 MTELPASPEFKANHAELMDEVVHWORHIYDVTRKYVLLGRDRLLDGLLEVPOGETVLELGC
 consensus 1 A HA LMDa Yr QRrIYDVTRr fLLGRDRLLI Ld P Ga VLEIaC

RsBtaB 53 GTGRNLDLIGRRAPGCRLSGLDISQEMLASARARLGRR-----ATLALGDATRFEEALPLF
 MlBtaB 61 GTGRNIIILAARRMPDARFFGLDISAEMLETAGKADREGLSGHVTLTRGDATDFEAAALY
 consensus 61 GTGRNl L gRRwP R GLDIS EML sA l R TL GDAT FeA Lf

RsBtaB 108 GTRFRFRTVLSYALSMIPDWREARREAAHLVPGCRLLHVDFGDOAGLPGWARACLRGWH
 MlBtaB 121 GIERFORMFVSYSLSMIPGWKKTUSAALAALSPNGSLHVDFGQQEGLPGWFRTLLRGWH
 consensus 121 G dRFeRi lSY LSMIP W l A L P G LHvVDFG Q GLPGW R LRGWi

RsBtaB 168 GRFHVTPRDLDGTALGETALGIGCYAEYRSLGCGYAILGTETR--
 MlBtaB 181 KKFHVTPRESLREVLESESRRTCATFRERILYRCYAWLAMTKIAS
 consensus 181 rFHVTPRd L L Gg yRsL GYA Lg l

FIGURE 21

Ml-*biaA* gene sequence

269421 atgacggacgtctcctcggatctggttttcgcgcggcaa
269461 ggaagttggaaaggccgtctaccagaaccgcgcgtttccaaagccggcatctccgagcg
269521 gctgttcgccttctgtttccggcctcgtctalccgcagatctgggaagaccccgatgt
269581 cgacatggaggccatgcagcttggtcagggccatcgcatcgtcacaatcgctccggcgg
269641 ctgcaacatcctcgcctacctcaccgttcgcgggcacggatcgacgccgtcgacctcaa
269701 cgccgccacatcgcgctgaaccgcatgaagctggaggcgggtgcgccgtcgcctcgcga
269761 gggcgatctgttcgcgtttttcggcgccgccgacaccagccacaattcgcaagcctatga
269821 ccgctttattgcgccgatctcgcgtcgggtcagccgccactattgggagcgccgcaactg
269881 gcgtggtcgccggcgcatcgccgtcttcgaccgcaatttctaccagaccggcctgctcgg
269941 cctgttcacgcctatggccatcgacggcgaaattcttcggcgtcaaccggcccacat
270001 gatggaagccaggaatatcggcgagcagcgccgttcttcaacaggagctggcgccggt
270061 cttcgacaagaagcttttgaaatgggcgacctcgcgtaaggcctcgctgttcggcctcgg
270121 cattccggcggcgagtagcattccctgatcacctcaggcgacggcaccatggccagcgt
270181 tctgaaggcccggctggaaaagctcgctgcgattttcccctggaaaacaattatttcgc
270241 ctggcaggcttttcccgcctatccaaatcccgggtgaggccgccctgcccgcctatct
270301 ggaaaagcagaactacgaaaccatccgcggcaatcgcaccgctcgccatccaccatgc
270361 caatctgatcgaattcctcgcggcaaggacgcgggcaccgtcgatcgcttcacctcgt
270421 cgatgcgcaggactggatgaccgatgaccagctcaacgcgctgttggtcggaaatcagccg
270481 caccgctccgcaggcgcccgctcattccgcaccgccgagcccagcctgctgcc
270541 aggcgcgctctcgacctcgtgctcgaccagtgggactatcaggacgaggcgtcgcgcga
270601 attctcggcacgcgaccgttcggccatctatggcggcttcacctctatgtgaagcgcac
270661 ggcatga

FIGURE 22

Ml-*btaB* gene sequence

270670 atgaccgagctgccggccagccccgaattcaaggccaatcatgccgaactg
270721 atggacggcgtctaccactggcagcgccacatctatgacctgactcgaaatactatctg
270781 ctcggccgcgaccggctgatcgaatgggcttgaggcgcaaggcggcaccgtgctggaa
270841 ctcggctgcggcaccggccgcaacatcatcctggccgcccgcgctaccctgatgcccgc
270901 ttcttcggcctggatatctcggccgagatgctggagacggccggcaaggcgatcgaccgc
270961 gaaggcctgtccggccacgtaacgctgacacgaggcgacgccaccgatttcgacggccgcg
271021 gcactttacggcatcgagcgcttcgaccgcgtcttcgtctcctattcgctgtcgaatgac
271081 ccaggctgggaaaagacgggtgtcggcgccactcgccgcactatccccaacggctcgctg
271141 cacatcgtcgatttcggccagcaggaaggcctaccgggctgggttcgtaccttgctgcgc
271201 ggttggctgaaaaattccacgtaacgccgcgtgaatcgctgcgcgaagtctggaatcg
271261 gaatctcggcgaaccggcgcaaccttcggttcgcacgctttatcgcggttacgcctgg
271321 ctggcgatgatcaagatgccagctaa

FIGURE 23

FIGURE 24

Agrobacterium tumefaciens BtaA DNA

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1 atg acg agt gcg gca ccc aag acc ggc ttc agc aaa aac acg aaa ctg aag tcc gca ttg
61 ctc cag cac aag gca ctc tcc aaa agc ggc ttc tcc gaa cgg ttt ttc ggc gtc ctc ttt
121 tcc ggc ctc gtc tat ccg cag atc tgg gaa gac ccc gag atc gac atg gaa gcg atg gag
181 ctt ggc gaa agc cac cgc atc gtc acc acc ggc ggc tgc aac atg cac atc gtc ggc tat
241 ctc tcg cgc aac ccg gtc agc atc gat gtc gat cat ctg gac ccc gag cac atc gtc ctg
301 aac aag ctg aag ctc gct ggc ttc cgc cat ctg ggt tat gac cat cag gat ttc atc gtc cac
361 ttc ggc cgc ggc acc aag gca tac agc aac agc gtc ggt cgc ggt ttc ggc gtc gag cat
421 ctg gat gcc acc ggc acc aag gca tac tgg tgg acc ggc cgc acc cgt ttc ggc cgt ggc
481 tcg gtc gcc acc ggc acc ggc gtc ggc ggc acc ggc cgt ttc ggc ggc ggc ggc ggc
541 cac atc atg gcc cgc cgc cgc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
601 gac gaa cag cgc cag cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc
661 ggc tgg ctg acg aag cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc
721 gac gag ctg gca agc ctt tcc aag agc tcc ggc ctt ggc att ggc ggc ggc ggc ggc ggc
781 gaa aag ctt gcc tgc agc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc
841 cgc cgt tat ccc gag cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc cgc
901 gaa aag atc cgc aac aac acc cat gag ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
961 ctt tcc cgc aag ccg cag gca aat ggc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc
1021 atg acg gat gtc cag ctc aac aat ggc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc
1081 gca cgc gtc atc ttc cgc cgc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
1141 gac atc cgc aac cag tgg ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
1201 cgc tcg gcc att tat ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc

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FIGURE 25

Agrobacterium tumefaciens BtaA protein

MTSAAPKTGFSKNTKLKSALLQHKALSKSGLSERFFGVLFSGLVYPQIWEDPEIDMEA
MELGEGHRIVTIGSGGCNMLAYLSRNPASIDVVDLNPHHIALNKLKLAAFRHLPAHQD
VVRHFGRAGTRSNSVGYDRFIAEHLDATTKAYWSKRTLSGRRRISVFDRNIYRTGLLG
RFIGAGHIMARLHGVKLTEMAKRTLDEQRQFFDSKVAPLFDKPVVRWLTKRKSSLFG
LGIPPRQYDELASLSSDGTVASVLKERLEKLACNFPLSDNYFAWQAFARRYPEPHEGA
LPAYLKPEYYEKIRNNTARVAVHHATYTELLSRKPANGVDRYILLDAQDWMTDVQLNE
LWSQISRTAASGARVIFRTAAEKSVIEGRLSPDIRNQWVYLEERSNELNAMDRSAIYG
GFHIYQRAMA

FIGURE 26

Agrobacterium tumefaciens BtaB DNA

```

1  atgaaaacca tgggcgagaa tgtcggcctt gcagacagcg cgcattgcggg cttgatggac
61  cgcattgtatc gccaccagcg ccatactctac gatatcaccg gcaaataatta tcttctgggc
121 cgtgaccgga ccatttcggg cctcgacgtg ccaaagggcg gcacgctgct ggaaatcggc
181 tgcggcaccg gccgcaacct gctgctggcc agccgccggg ttcccgacgc caaactcttc
241 ggcttcgata tatcagccga aatgctgctg accgcctccg agaattttgc cggcaaagcg
301 gagcgaccca ttctgctgtg cgccgatgcc accgctttcc ggtcttcgga attcggccag
361 cccgatggct tcgaccgcgt catgatccct tatgcgctgt cgatgatacc ggactgggaa
421 aaagcgatcg aacaggcgct cgcggcgctg aaaccggcg gttcgctgca tatcgtcgat
481 ttcggccagc aggaacagtt gccgaagtgg ttccgcacgc ttcttcaagc ctggctcacc
541 cgctttcacg ttacgccccg cgcaaatctc cgttacgttc tcgccaatat ggccggccgt
601 ttcgacggga atctcgtctt cgaggaaatc gcgaggggat acgcatggcg ggctgtcatc
661 acgcttccgg ttgccgaagc cccgcagccg aagatccacc gcttattggc tgacgcctga

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FIGURE 27

Agrobacterium tumefaciens BtaB protein

MTDATHAALMDATYRHQRRYDVTRRHFLGRDRLIAELDPPPG
ARVLEIACGTGRNLDLIGRRWPGCRLSGLDISQEMLASARARLG
RRATLALGDATRFEALPLFGTDRFERIVLSYALSMIPDWREALR
EAALHLVPGGRLHVVDGQAGLPGWARAGLRGWIGRFHVTPRD
DLGTALGETALGIGGYAEYRSLGGGYAILGTLTR

FIGURE 28

Sinorhizobium meliloti BtaA DNA

[illegible]

FIGURE 29

Sinorhizobium meliloti BtaA protein

MTDFAPDAGFGKKNPKLKSALLQHKALSPAGLSERLFGLLFSGLVYPQIWEDPIVDME
AMQIRPGHRIVTIGSGGCNMLTYLSAEPARIDVVDLNPHHIALNRLKLSAFRHLP SHK
DVVRFLAVEGTRTNGQAYDVFLAPKLDPATRAYWNGRDLTGRRRIGVFGRNVYRTGLL
GRFISASHALARLHGINPEDFVKARSMREQRQFFDDKLAPL FERPVIRWITSRKSSLF
GLGIPPQQFDELASLSREKSVAAVLRNRLEKLTCHFPLRDNYFAWQAFARRYPRPDEG
ELPPYLQASRYEAIRDNAERVEVHHASFTELLAGKPAASVDRYVLLDAQDWMTDQQLN
DLWTEITRTADAGAVVIFRTAAEASILPGRLSTTLLDQWYYDAETSMRLGAEDRSAIY
GGFHIYRKKA

FIGURE 30

Sinorhizobium meliloti BtaB DNA

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1  atgagcgccg tgcagaccgc gaatgaaagc cacgctcatc tgatggaccg catgtatcgc
61 taccagcggc acatctatga ttccactcgc aaatactatc tcttcggccg tgacacgctg
121 atccgtgaac tgaacccgcc gccaggcgca tcggtgctgg aagtcggctg cggcacgggc
181 cgcaatctcg ccgtgatcgg ggatctctac cccggtgcgc gcctcttcgg cctcgatata
241 tcggccgaaa tgctggcgac cgccaaagcc aagctccggc gccaaaatcg gccggacgca
301 gtggtgcggg tcgccgacgc gacgaatttc accgccgcct cattcgatca ggaaggcttc
361 gaccggatcg tcatttccta cgccctttcc atggttcccg aatgggaaaa ggcggtcgat
421 gccgcgattg ccgcgctcaa gccggggcggc tcgctgcata tcgccgactt cggccagcag
481 gaaggttggc cggccggcct ccgccgcttc ctccaggcct ggctcagacg cttccacgtc
541 acgccgcgcg aaacgccttt cgatgtgatg cgcaaaagag ccgagagaaa cggagcggcg
601 ctcgaggtca gatcgctgag acgaggttat gcctggcttg tcgtctatcg ccgcgcggca
661 ccgtag

```

FIGURE 31

Sinorhizobium meliloti BtaB protein

MSAVQTANESHAPLMDRMYRYQRYIYDFTRKYYLFGRDTLIREL
NPPPGASVLEVCGGTGRNLAVIGDLYPGARLFGLDISAEMPLATA
KAKLRRQNRPDVLRVADATNFTAASFDQEGFDRIVISYALSMV
PEWEKAVDAAIAALKPGGSLHIADFGQEGWPAGFRRFLQAWLR
RFHVTPRETLDVMRKRAERNGAALEVRSLLRGYAWLVVYRRAA
P

Figure 32

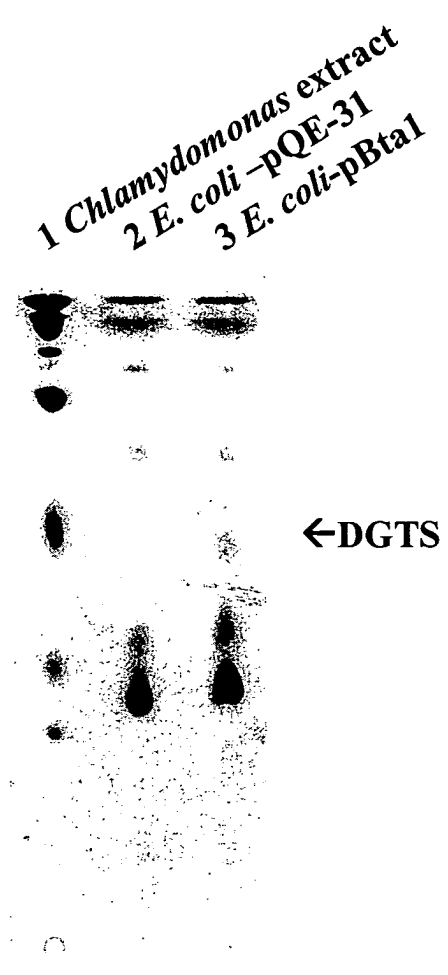


Figure 33

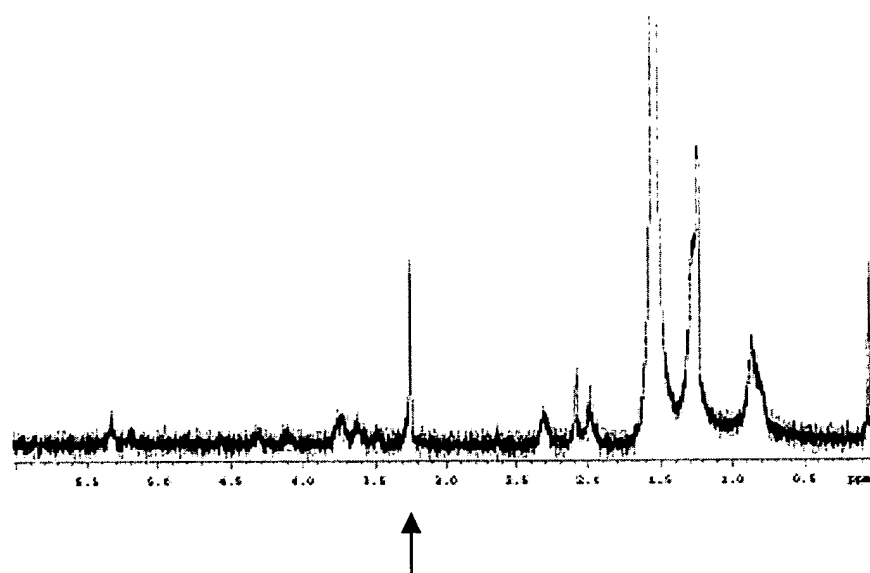
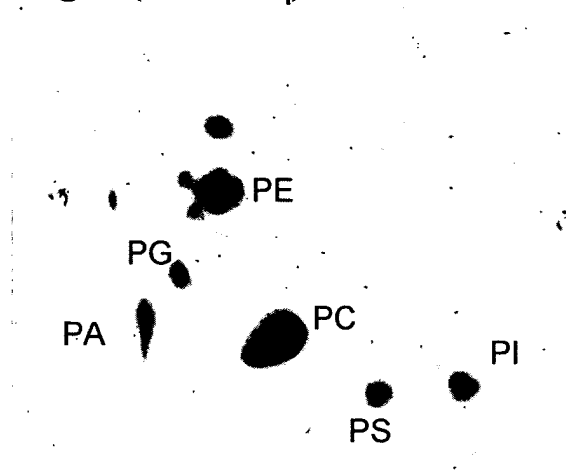


Figure 34

A. Vogels (20 mM P_i)



B. Vogels -P +MES (0.01 mM P_i)

